

**BLASTP 2.2.6 [Apr-09-2003]**

RID: 1067455426-9658-2307585.BLASTQ3

Query=

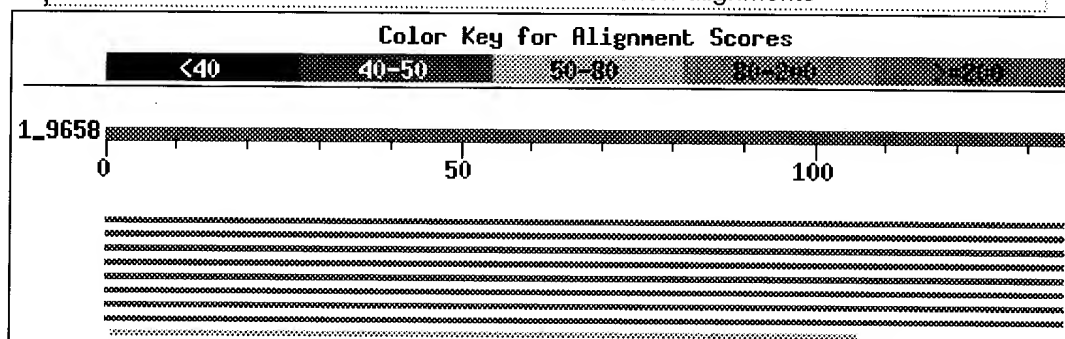
(136 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

1,530,482 sequences; 497,137,717 total letters

Taxonomy reports**Distribution of 355 Blast Hits on the Query Sequence**








Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 284667 pir A43427	neurofilament triplet H1 protein - ra...	334	1e-90	
gi 71549 pir QFHUH	neurofilament triplet H protein - human...	325	5e-88	
gi 32483416 ref NP_066554.2 	neurofilament, heavy polypepti...	325	5e-88	
gi 33302611 sp P12036 NFH_HUMAN	Neurofilament triplet H pro...	322	3e-87	
gi 27529742 dbj BAA74868.2 	KIAA0845 protein [Homo sapiens]	322	3e-87	
gi 601931 gb AAA57153.1 	neurofilament-H	317	1e-85	
gi 284668 pir B43427	neurofilament protein H form H2 (repe...	313	2e-84	
gi 24020878 gb AAN40837.1 AF346625.1	heavy neurofilament pr...	309	3e-83	
gi 21429606 gb AAM49796.1 	heavy neurofilament NF-H [Rattus...	271	8e-72	
gi 205686 gb AAA41695.1 	heavy neurofilament subunit	271	8e-72	
gi 14250426 gb AAH08648.1 AAH08648	Unknown (protein for IMA...	270	1e-71	
gi 128127 sp P19246 NFH_MOUSE	Neurofilament triplet H prote...	270	2e-71	
gi 28972433 dbj EAC65670.1 	mKIAA0845 protein [Mus musculus]	270	2e-71	
gi 29789026 ref NP_036739.1 	neurofilament, heavy polypepti...	268	8e-71	
gi 205680 gb AAA41692.1 	high molecular weight neurofilament	268	8e-71	

gi 200022 gb AAA39809.1 neurofilament protein >gi 226537 p...	267	1e-70	
gi 463250 emb CAA83229.1 Neurofilament protein, high molec...	267	1e-70	
gi 92538 pir S02003 neurofilament triplet H protein - rat ...	245	6e-64	
gi 462702 sp P16884 NFM RAT Neurofilament triplet H protein...	245	6e-64	
gi 37549256 ref XP_291369.3 similar to KIAA0845 protein [H...	207	1e-52	
gi 13629976 sp O77788 NFM BOVIN Neurofilament triplet M pro...	152	8e-36	
gi 226213 prf 1501343A neurofilament protein NF-H C term	147	2e-34	
gi 1160355 gb AAB00542.1 UNC-89	136	4e-31	
gi 7511618 pir T29757 protein UNC-89 - Caenorhabditis elegans	136	4e-31	
gi 31746683 gb AAP68958.1 Uncoordinated protein 89, isoform...	136	4e-31	
gi 25141314 ref NP_491290.2 UNCoordinated locomotion UNC-8...	136	4e-31	
gi 4885513 ref NP_005373.1 neurofilament 3 (150kDa medium)...	113	2e-24	
gi 6003540 gb AAF00492.1 AF181990.1 neurofilament-3 (150 kD...	111	1e-23	
gi 14149397 gb AAK54495.1 AF368231.2 neurofilament triplet ...	102	9e-21	
gi 423935 pir A46194 neurofilament protein NF-220, high-mo...	101	1e-20	
gi 18767706 ref NP_571997.1 neurofilament triplet H1-like ...	101	2e-20	
gi 14549637 gb AAK66966.1 AF255740.1 histone H1 [Bufo bufo ...	97	2e-19	
gi 23469403 ref ZP_00124737.1 COG3064: Membrane protein in...	92	1e-17	
gi 32966575 gb AAP92164.1 histone H1 [Medicago truncatula]	92	1e-17	
gi 13540405 gb AAK29456.1 AF352253.1 histone H1 [Lens culin...	91	1e-17	
gi 13540403 gb AAK29455.1 AF352252.1 histone H1 [Lens culin...	91	1e-17	
gi 2981173 gb AAC06245.1 neurofilament medium subunit [Ser...	90	3e-17	
gi 13540395 gb AAK29451.1 AF352248.1 histone H1 [Pisum sati...	90	3e-17	
gi 128146 sp P16053 NFM CHICK Neurofilament triplet M prote...	90	3e-17	
gi 63686 emb CAA29073.1 NF-M c-terminus [Gallus gallus]	90	3e-17	
gi 7439660 pir T06257 histone H1 (clone TH32) - wheat >gi ...	89	8e-17	
gi 21465095 gb AAM54671.1 AF514417.1 histone H1 [Pisum sati...	88	1e-16	
gi 4106696 dbj BAA36284.1 ribosome-sedimenting protein [Pi...	88	1e-16	
gi 4996567 dbj BAA78535.1 ribosome-sedimenting protein [Pi...	88	1e-16	
gi 21465093 gb AAM54670.1 AF514416.1 histone H1 [Lathyrus a...	88	2e-16	
gi 13540401 gb AAK29454.1 AF352251.1 histone H1 [Lens culin...	88	2e-16	
gi 13540391 gb AAK29449.1 AF352246.1 histone H1 [Pisum sati...	87	3e-16	
gi 13540397 gb AAK29452.1 AF352249.1 histone H1 [Lathyrus s...	87	4e-16	
gi 13540399 gb AAK29453.1 AF352250.1 histone H1 [Lathyrus s...	87	4e-16	
gi 30420974 gb AAP31307.1 histone H1 [Lens nigricans]	87	4e-16	
gi 805006 emb CAA56558.1 pprB [Pseudomonas putida]	87	4e-16	
gi 28867376 ref NP_789995.1 alginate regulatory protein Al...	85	2e-15	
gi 9630970 ref NP_047640.1 mucin-like protein [Lymantria d...	83	5e-15	
gi 13540393 gb AAK29450.1 AF352247.1 histone H1 [Pisum sati...	83	7e-15	
gi 16127671 ref NP_422235.1 arylesterase-related protein [...	82	9e-15	
gi 2114317 dbj BAA20035.1 tegument protein [Equine herpesv...	82	1e-14	
gi 5230788 gb AAD41008.1 AF107026.1 histone H1 WH1A.3 [Trit...	81	2e-14	
gi 5230790 gb AAD41009.1 AF107027.1 histone H1 WH1A.4 [Trit...	81	2e-14	
gi 7439656 pir T06241 histone H1 (clone TH315) - wheat >gi ...	81	2e-14	
gi 30420972 gb AAP31306.1 histone H1 [Vicia hirsuta]	80	4e-14	
gi 14916992 sp P27806 H1 WHEAT Histone H1	80	4e-14	
gi 11558848 emb CAA42529.2 histone H1 [Triticum aestivum]	80	4e-14	
gi 5230781 gb AAD41005.1 AF107022.1 histone H1 WH1A.1 [Trit...	80	4e-14	
gi 5230783 gb AAD41006.1 AF107023.1 histone H1 WH1A.2 [Trit...	80	5e-14	
gi 7428714 pir QFPGM neurofilament triplet M protein - pig...	79	7e-14	
gi 26986938 ref NP_742363.1 alginate regulatory protein Al...	79	7e-14	
gi 283442 pir A40215 TcD antigen - Trypanosoma cruzi	79	1e-13	
gi 161958 gb AAB97874.1 surface antigen [Trypanosoma cruzi]	78	1e-13	
gi 31213063 ref XP_315475.1 ENSANGP00000021721 [Anopheles ...	78	2e-13	
gi 28209501 gb AAO37519.1 histone-like protein [Oryza sati...	77	3e-13	
gi 22963111 ref ZP_00010717.1 COG3064: Membrane protein in...	77	4e-13	
gi 283024 pir S22322 histone H1 - wheat	74	3e-12	
gi 2118971 pir I51227 histone H1A - African clawed frog >g...	73	4e-12	

gi 2623960 emb CAA73171.1 	histone H1 [Apium graveolens]	72	8e-12	
gi 15217879 ref NP_174150.1 	prolin-rich protein -related [...]	72	1e-11	
gi 30018740 ref NP_830371.1 	Internalin protein [Bacillus c...]	71	1e-11	
gi 29561775 emb CAD87780.1 	SI:dZ258D18.1 (novel protein si...)	71	2e-11	
gi 15602833 ref NP_245905.1 	TolA [Pasteurella multocida] >...	71	2e-11	
gi 121955 sp P02254 H1_SALTR	Histone H1 >gi 70667 pir HSTR...	71	2e-11	
gi 2133786 pir I51116	NF-180 - sea lamprey >gi 632549 gb A...	71	2e-11	
gi 121922 sp P06893 H1B_XENLA	HISTONE H1B >gi 2118972 pir ...	70	5e-11	
gi 70670 pir HSXL1B	histone H1B - African clawed frog	70	5e-11	
gi 23054984 ref ZP_00081113.1 	COG0532: Translation initiat...	69	6e-11	
gi 25143299 ref NP_492875.2 	pre-mRNA splicing SR protein r...	69	6e-11	
gi 9626761 ref NP_041033.1 	tegument protein [Equine herpes...]	69	8e-11	
gi 22538198 ref NP_689049.1 	pathogenicity protein, putativ...	69	8e-11	
gi 2114319 dbj BAA20036.1 	tegument protein [Equine herpesv...]	69	8e-11	
gi 5230785 gb AAD41007.1 AF107024.1	histone H1 WH1B.1 [Trit...	68	2e-10	
gi 121951 sp P06350 H1_ONCMY	Histone H1 [Contains: Oncorhyn...	68	2e-10	
gi 70668 pir HSTR1R	histone H1 - rainbow trout	68	2e-10	
gi 121918 sp P06892 H1A_XENLA	HISTONE H1A >gi 64775 emb CAA...	67	3e-10	
gi 482295 pir A36128	regulatory protein algP - Pseudomonas...	67	3e-10	
gi 70669 pir HSXL1A	histone H1A - African clawed frog	67	3e-10	
gi 15600446 ref NP_253940.1 	alginate regulatory protein Al...	66	5e-10	
gi 30420970 gb AAP31305.1 	histone H1 [Vicia faba]	66	7e-10	
gi 4885381 ref NP_005313.1 	H1 histone family, member 5 [Ho...	66	7e-10	
gi 25012056 ref NP_736451.1 	putative peptidoglycan linked ...	66	9e-10	
gi 22597168 gb AAN03471.1 	unknown protein [Glycine max]	66	9e-10	
gi 108359 pir S02571	neurofilament triplet protein H - pig...	65	1e-09	
gi 21426893 ref NP_064418.1 	histone 1, H1b; histone 1, fam...	65	2e-09	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|284667|pir||A43427](#) neurofilament triplet H1 protein - rabbit (fragment)
[gi|601930|gb|AAA57152.1|](#) neurofilament-H
 Length = 606

Score = 334 bits (781), Expect = 1e-90

Identities = 133/189 (70%), Positives = 134/189 (70%), Gaps = 53/189 (28%)

Query: 1 AKSPAE-----AKSPAEAKSP-----AKSPAEAKSPEKAKSP--- 32
 AKSP E AKSPAEAKSP AKSPAEAKSPEKAKSP
 Sbjct: 39 AKSPTEGGAASPEEEAKSPAEAKSPVKEEAKSPAEAKSPAEAKSPAEAKSPEKAKSPVKE 98

Query: 33 -AKSPAEAKSPVKEEAKSP--AKSPEKAKSPAEAKSP-----AKSPEK-----A 73
 AKSP +AKSPVKEEAKSP AKSPEKAKSPAEAKSP AKSPEK A
 Sbjct: 99 EAKSPEKAKSPVKEEAKSPAEAKSPEKAKSPAEAKSPEKAKSPVKEEAKSPEKAKSPA EA 158

Query: 74 KSPEKAKSP--AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPAEAKSP--AKSPVKEEA 127
 KSPEKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSPAEAKSP AKSPVKEEA
 Sbjct: 159 KSPEKAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPA EAKSPEKAKSPVKEEA 218

Query: 128 KSPEKAKSP 136
 KSPEKAKSP
 Sbjct: 219 KSPEKAKSP 227

Score = 326 bits (763), Expect = 2e-88

Identities = 132/194 (68%), Positives = 134/194 (69%), Gaps = 58/194 (29%)

Query: 1 AKSPA EAKSP-----AEAKSPA--KSPA EAKSPEKAKSP----AKSPA EAKSPVKEE 46
AKSPA EAKSP AEAKSPA KSPA EAKSPEKAKSP AKSP +AKSPVKEE
Sbjct: 54 AKSPA EAKSPVKEEAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEE 113

Query: 47 AKSPA--KSPEKAKSPA EAKSP-----AKSPEKAKSP----- 76
AKSPA KSPEKAKSPA EAKSP AKSPEKAKSP
Sbjct: 114 AKSPA EAKSPEKAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPA EAKSPA EAKSPA EAKSPA 173

Query: 77 EKAKSP---AKSPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSP--AKSP 122
EKAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSP
Sbjct: 174 EKAKSPVKEEAKSPEKAKSPVKEEAKSPA EAKSPA EAKSPA EAKSPVKEEAKSPEKAKSPA EAKSPA 233

Query: 123 VKEEAKSPEKAKSP 136
VKEEAKSPEKAKSP
Sbjct: 234 VKEEAKSPEKAKSP 247

Score = 307 bits (717), Expect = 1e-82

Identities = 134/246 (54%), Positives = 134/246 (54%), Gaps = 110/246 (44%)

Query: 1 AKSPA EAKSPA-----EAKSP-----AKSPA EAKSPEKAKSP----- 32
AKSPA EAKSP EAKSP AKSPA EAKSPEKAKSP
Sbjct: 164 AKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPA EAKSPA EAKSPA EAKSPA EAKSPA EAKSPA 223

Query: 33 AKSPA EAKSPVKEEAKSP-----AKSPEKAKSP-----AEAK 64
AKSPA EAKSPVKEEAKSP AKSPEKAKSP AEAK
Sbjct: 224 AKSPA EAKSPVKEEAKSPEKAKSPEKEEAKSPA EAKSPA EAKSPA EAKSPA EAKSPA EAKSPA 283

Query: 65 SP-----AKSPEKAKSP-----EKAKSP---AKSPEK 88
SP AKSPEKAKSP EKAKSP AKSPEK
Sbjct: 284 SPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 343

Query: 89 AKSPVKEEAKSP--AKSPVKEEAKSPA-----EAKSP--AKSPVKEEAKSP 130
AKSPVKEEAKSP AKSPVKEEAKSP EAKSP AKSPVKEEAKSP
Sbjct: 344 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 403

Query: 131 EKAKSP 136
EKAKSP
Sbjct: 404 EKAKSP 409

Score = 240 bits (559), Expect = 2e-62

Identities = 117/238 (49%), Positives = 120/238 (50%), Gaps = 104/238 (43%)

Query: 1 AKSPA EAKSPA EAKSP--AKSPA--EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP-- 50
AKSP E KSPA EAKSP AKSP EAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 270 AKSPVEVKSPA EAKSPA EAKSPA EAKSPA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 329

Query: 51 -----AKSPEKAKSPA--EAKSP-----AKSPEKAKSPEKAKSP----- 82
AKSPEKAKSP EAKSP AKSPEKAKSPEKAKSP
Sbjct: 330 AKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSP 389

Query: 83 -----AKSPEKAKSPVKEEAKSPA K-SPVKEEAK----- 110

10/29/03

EKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAK
Sbjct: 692 EKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAK 751

Query: 135 SP 136
SP
Sbjct: 752 SP 753

Score = 316 bits (738), Expect = 3e-85
Identities = 131/202 (64%), Positives = 132/202 (65%), Gaps = 66/202 (32%)

Query: 1 AKSPAE-----AKSPAEAKSP-----AKSPAE 22
AKSPAE AKSP EAKSP AKSPAE
Sbjct: 538 AKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA 597

Query: 23 AKSPEKAKSP----AKSPAEAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPAEAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 598 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 657

Query: 73 --AKSPEKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
AKSPEKAKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP EAK
Sbjct: 658 EEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAK 717

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAK+PEKAKSP
Sbjct: 718 SPEKAKSPVKEEAKTPEKAKSP 739

Score = 309 bits (723), Expect = 3e-83
Identities = 130/196 (66%), Positives = 130/196 (66%), Gaps = 60/196 (30%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50
AKSP EAKSPA EAKSP AKSPA KSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 516 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 576 AEVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 635

Query: 77 EKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAKSP--AK 120
EKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAKSP AK
Sbjct: 636 EKAKSPTKEEAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAK 695

Query: 121 SPVKEEAKSPEKAKSP 136
SPVKEEAKSPEKAKSP
Sbjct: 696 SPVKEEAKSPEKAKSP 711

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPA KSPA E--AKSPEK--AKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA-- 61
E KSP PAE A SPEK AKSP AKSPA EAKSP KEEAKSPA KSPEKAKSPA
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KE 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP-- 100
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP

Sbjct: 557 EAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPA EAKSP--AKSPVKEEAKSPEKAKSP 136
AKSPVKEEAKSPA E KSP AKSP KEEAKSPEKAKSP

Sbjct: 617 EAKSPVKEEAKSPA EVKSPEKAKSP TKEEAKSPEKAKSP 655

Score = 261 bits (608), Expect = 1e-68

Identities = 121/235 (51%), Positives = 124/235 (52%), Gaps = 99/235 (42%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50
AKSP EAKSPA EAKSP AKSPA E KSPEKAKSP AKSP +AKSP KEEAKSP

Sbjct: 604 AKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSP TKEEAKSPEKAKSPEKEEAKSP 663

Query: 51 -----AKSPEKAKSP--AEAKSP-----AKSPEKAKSP-----EKAK 80
AKSPEKAKSP AEAKSP AKSPEKAKSP EKAK

Sbjct: 664 EKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAK 723

Query: 81 SP----AKSPEKAKSPVKEEAKSP----- 100
SP AK+PEKAKSPVKEEAKSP

Sbjct: 724 SPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PADKFPE 783

Query: 101 -AKSPVKEEAKSPA EAKSP-----AKSPVKEEAKSPE-KAKSP 136
AKSPVKEE KSP +AKSP KSPVKEE K E K K P

Sbjct: 784 KAKSPVKEEVKSPEKAKSPLKADAKAPEKEI PKKEEVKSPVKEEEKPQEVKVKEP 838

Score = 210 bits (488), Expect = 3e-53

Identities = 117/272 (43%), Positives = 124/272 (45%), Gaps = 139/272 (51%)

Query: 1 AKSPA EAKSP--AEAKSP--AKSP--AEAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP

Sbjct: 660 AKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 719

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAK-----SPEKAKSPA K-----SP- 86
AK+PEKAKSP EAKSP AKSPEKAK SPE AK+PAK SP

Sbjct: 720 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPE-AKTPAKEEARS PA 778

Query: 87 -----EKAKSPVKEE-----AKSP-----AKSPVKE----- 107
EKAKSPVKEE AKSP KSPVKE

Sbjct: 779 DKFPEKAKSPVKEEVKSPEKAKSPLKADAKAPEKEI PKKEEVKSPVKEEEKPQEVKVKEP 838

Query: 108 -----EAKSPA-----EAK----- 116
E K+PA EAK

Sbjct: 839 PKKAE E E K A P A T P K T E E K D S K K E E A P K K E A P K P K V E E K K E P A V E K P K E S K V E A K K E E A E 898

Query: 117 -----SPA KSPVKEEAKSPEK---AK 134
+PAK VKE+AK EK AK

Sbjct: 899 DKKKVPTPEKEAPAKVEVKEDAKPKTEKTEVAK 930

Score = 100 bits (229), Expect = 3e-20

Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPA EAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP----AKSPA-----EA 39
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E

Sbjct: 762 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKADAKAPEKEI PKKEEV 820

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
 KSPVKE E K+PA K+ EK A K P
 Sbjct: 821 KSPVKEEEKPQEVKVKEPPKAAEEKAPATPKTEEEKKDSKKEEAPKKEAPKPKVVEEKKEP 880

Query: 61 A-----EAK-----SPAK-----SP-EKA----KSPE--KAKS 81
 A EAK +PAK P EK K P+ KAK
 Sbjct: 881 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKTEVAKKEPDDAKAKE 940

Query: 82 PAKSPEKAKSPVKEEAKSPAKSPVKEE-AKSPAE-AKSPAKSPVKEEAKS----P----- 130
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
 Sbjct: 941 PSKPAEK-----KEAA--PEKKDTKEEKAKKPPEEKPKTEAKA--KEDDKTLSKEPSKPKA 991

Query: 131 EKA-KS 135
 EKA KS
 Sbjct: 992 EKAES 997

Score = 97.8 bits (223), Expect = 2e-19
 Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPAIAKSP---AKSPVKEEAKSPEKAKSP 136
 E+ KSP EEA SP AKSPVKEEAKSPAIAKSP AKSP E KSPEKAKSP
 Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPAIAKSPKEKEEAKSP--AEVKSPEKAKSP 553

gi|32483416|ref|NP_066554.2 neurofilament, heavy polypeptide 200kDa; Neurofi
 polypeptide; neurofilament, heavy polypeptide (200kD)
 [Homo sapiens]
 Length = 1020

Score = 325 bits (760), Expect = 5e-88
 Identities = 130/182 (71%), Positives = 132/182 (72%), Gaps = 46/182 (25%)

Query: 1 AKSPAIAKSPAIAKSPAK----SPAIAKSPEKAKSP----AKSPAIAKSPVKEEAKSPA- 51
 AKSPAIA KSP +AKSPA SPAIAKSPEKAKSP AKSPAIAKSPVKEEAKSPA
 Sbjct: 572 AKSPAIVKSPEKAKSPAIAKSPAIAKSPEKAKSPVKEEAKSPAIAKSPVKEEAKSPAIA 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EAKSP----AKSP 86
 KSPEKAKSP EAKSP AKSPEKAKSP EAKSP AKSP
 Sbjct: 632 VKSPEKAKSPTEKAKSPAIAKSPEKAKSPAIAKSPEKAKSPVKAIAKSPEKAKSPVKAIAKSP 691

Query: 87 EKAKSPVKEEAKSP--AKSPVKEEAKSPAIAKSP-----AKSPVKEEAKSPEKAK 134
 EKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAK
 Sbjct: 692 EKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAK 751

Query: 135 SP 136
 SP
 Sbjct: 752 SP 753

Score = 316 bits (738), Expect = 3e-85
 Identities = 131/202 (64%), Positives = 132/202 (65%), Gaps = 66/202 (32%)

Query: 1 AKSPAIA-----AKSPAIAKSP-----AKSPAIA 22
 AKSPAIA AKSP EAKSP AKSPAIA
 Sbjct: 538 AKSPAIVKSPEKAKSPAIAKSPAIAKSPAIAKSPAIAKSPAIAKSPAIAKSPAIAKSPAIA 597

Query: 23 AKSPEKAKSP----AKSPAEAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPAEAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 598 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 657

Query: 73 --AKSPEKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
AKSPEKAKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP EAK
Sbjct: 658 EEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAK 717

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAK+PEKAKSP
Sbjct: 718 SPEKAKSPVKEEAKTPEKAKSP 739

Score = 309 bits (723), Expect = 3e-83

Identities = 130/196 (66%), Positives = 130/196 (66%), Gaps = 60/196 (30%)

Query: 1 AKSPA--EAKSPAEAKSP----AKSPAEAKSPEKAKSP----AKSPAEAKSPVKEEAKSP 50
AKSP EAKSPAEAKSP AKSPA EKSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 516 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 576 AEVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 635

Query: 77 EKAKSP----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAKSP--AK 120
EKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAKSP AK
Sbjct: 636 EKAKSPTKEEAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAK 695

Query: 121 SPVKEEAKSPEKAKSP 136
SPVKEEAKSPEKAKSP
Sbjct: 696 SPVKEEAKSPEKAKSP 711

Score = 280 bits (653), Expect = 2e-74

Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPA KSPA E--AKSPEK--AKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA-- 61
E KSP PAE A SPEK AKSP AKSPA EAKSP KEEAKSPA KSPEKAKSPA
Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KE 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP- 100
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP
Sbjct: 557 EAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPA EAKSP--AKSPVKEEAKSPEKAKSP 136
AKSPVKEEAKSPA E KSP AKSP KEEAKSPEKAKSP
Sbjct: 617 EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSP 655

Score = 228 bits (531), Expect = 8e-59

Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPA EAKSP--AEAKSP--AKSP--AEAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 660 AKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 719

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75
AK+PEKAKSP EAKSP AKSPEKAK+
Sbjct: 720 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PAD 779

Query: 76 --PEKAKSPAK----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSPAK 120
PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K
Sbjct: 780 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPVKEEEK-PQEVK---- 834

Query: 121 SPVKEEAKSPEKAKSP 136
VKE K E+ K+P
Sbjct: 835 --VKEPPKKA EEEKAP 848

Score = 100 bits (229), Expect = 3e-20
Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPA EAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP---AKSPA-----EA 39
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E
Sbjct: 762 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 820

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
KSPVKE E K+PA K+ EK A K P
Sbjct: 821 KSPVKEEEKPQEVKVKEPPKKA EEEKAPATPKTEEEKDSKKEEAPKKEAPKPKVEEKKEP 880




Query: 61 A-----EAK-----SPAK-----SP-EKA----KSPE--KAKS 81
A EAK +PAK P EK K P+ KAK
Sbjct: 881 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 940

Query: 82 PAKSPEKAKSPVKEEAKSPA KSPVKEE-AKSPA E-AKSPA KSPVKEEAKS----P----- 130
P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
Sbjct: 941 PSKPAEK-----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 991

Query: 131 EKA-KS 135
EKA KS
Sbjct: 992 EKA EKS 997

Score = 97.8 bits (223), Expect = 2e-19
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA EAKSP---AKSPVKEEAKSPEKAKSP 136
E+ KSP EEA SP AKSPVKEEAKSPA EAKSP AKSP E KSPEKAKSP
Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSP--AEVKSPEKAKSP 553

 >gi|33302611|sp|P12036|NFH HUMAN  Neurofilament triplet H protein (200 kDa neur
(Neurofilament heavy polypeptide) (NF-H)
gi|6470331|gb|AAF13722.1|AF203032.1  neurofilament protein [Homo sapiens]
Length = 1026

Score = 322 bits (754), Expect = 3e-87
Identities = 130/188 (69%), Positives = 132/188 (70%), Gaps = 52/188 (27%)

Query: 1 AKSPA EAKSPA EAKSPA K---SPA EAKSPEKAKSP---AKSPA EAKSPVKEEAKSPA- 51
AKSPA E KSP +AKSPA SPA EAKSPEKAKSP AKSPA EAKSPVKEEAKSPA
Sbjct: 572 AKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA E 631

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKAKSP-- 82
KSPEKAKSP EAKSP AKSPEKAKSP EKAKSP
Sbjct: 632 VKSPEKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKAEAKSPEKAKSPVK 691

Query: 83 --AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPA EAKSP-----AKSPVKEEAK 128
AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAK
Sbjct: 692 AEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAK 751

Query: 129 SPEKAKSP 136
SPEKAKSP
Sbjct: 752 SPEKAKSP 759

Score = 313 bits (732), Expect = 2e-84
Identities = 131/208 (62%), Positives = 132/208 (63%), Gaps = 72/208 (34%)

Query: 1 AKSPA E-----AKSPA EAKSP-----AKSPA 22
AKSPA AKSP EAKSP AKSPA
Sbjct: 538 AKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA 597

Query: 23 AKSPEKAKSP---AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPA EAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 598 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 657

Query: 73 AKSPEK--AKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP----- 112
AKSPEK AKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP
Sbjct: 658 AKSPEKEEAKSPEKAKSPVKAEAKSPEKAKSPVKAEAKSPEKAKSPVKEEAKSPEKAKSP 717

Query: 113 --AEAKSP--AKSPVKEEAKSPEKAKSP 136
EAKSP AKSPVKEEAK+PEKAKSP
Sbjct: 718 VKEEAKSPEKAKSPVKEEAKTPEKAKSP 745

Score = 307 bits (717), Expect = 1e-82
Identities = 130/202 (64%), Positives = 130/202 (64%), Gaps = 66/202 (32%)

Query: 1 AKSPA--EAKSPA EAKSP---AKSPA EAKSPEKAKSP---AKSPA EAKSPVKEEAKSP 50
AKSP EAKSPA EAKSP AKSPA KSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 516 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 575

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 576 AEVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 635

Query: 77 EKAKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
EKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAK
Sbjct: 636 EKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKAEAKSPEKAKSPVKAEAK 695

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAKSPEKAKSP
Sbjct: 696 SPEKAKSPVKEEAKSPEKAKSP 717

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPAKSPAE-AKSPEK-AKSP----AKSPAEAKSPVKEEAKSPA--KSPEKAKSPA-- 61
 E KSP PAE A SPEK AKSP AKSPAEAKSP KEEAKSPA KSPEKAKSPA
 Sbjct: 500 ETKSP---PAEEAASPEKEAKSPVKEEAKSPAEAKSPEKEEAKSPAENVKSPEKAKSPA 556

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP- 100
 EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP
 Sbjct: 557 EAKSPPEAKSPEKEEAKSPAENVKSPEKAKSPAEEAKSPAEEAKSPEKAKSPVKEEAKSPA 616

Query: 101 -AKSPVKEEAKSPAEAKSP--AKSPVKEEAKSPEKAKSP 136
 AKSPVKEEAKSPA KSP AKSP KEEAKSPEKAKSP
 Sbjct: 617 EAKSPVKEEAKSPAENVKSPEKAKSPTEKEEAKSPEKAKSP 655

Score = 228 bits (531), Expect = 8e-59

Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPAEAKSP--AEAKSP--AKSP--AEAKSPEKAKSP----AKSPAEAKSPVKEEAKSP 50
 AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP
 Sbjct: 666 AKSPEKAKSPVKAEEAKSPEKAKSPVKAEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 725

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75
 AK+PEKAKSP EAKSP AKSPEKAK+
 Sbjct: 726 EAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PAD 785

Query: 76 --PEKAKSPAK----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSPAK 120
 PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K
 Sbjct: 786 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPVKEEEK-PQEVK---- 840

Query: 121 SPVKEEAKSPEKAKSP 136
 VKE K E+ K+P
 Sbjct: 841 --VKEPPKAE EEEKAP 854

Score = 100 bits (229), Expect = 3e-20

Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPAEAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP----AKSPA-----EA 39
 KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E
 Sbjct: 768 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 826

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
 KSPVKE E K+PA K+ EK A K P
 Sbjct: 827 KSPVKEEEKPQEVKVKEPPKKAEEEEKAPATPKTEEEKKDSKKEEAPKKEAPKPKVVEEKKEP 886

Query: 61 A-----EAK-----SPAK-----SP-EKA----KSPE--KAKS 81
 A EAK +PAK P EK K P+ KAK
 Sbjct: 887 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 946

Query: 82 PAKSPEKAKSPVKEEAKSPA KSPVKEE-AKSPA E-AKSPA KSPVKEEAKS-----P----- 130
 P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
 Sbjct: 947 PSKPAEK-----KEAA--PEKKDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 997

Query: 131 EKA-KS 135
 EKA KS
 Sbjct: 998 EKA EKS 1003

Score = 97.8 bits (223), Expect = 2e-19
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA EAKSP---AKSPVKEEAKSPEKAKSP 136
E+ KSP EEA SP AKSPVKEEAKSPA EAKSP AKSP E KSPEKAKSP
Sbjct: 499 EETKSPPAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSP--AEVKSPEKAKSP 553

 >gi|27529742|dbj|BAA74868.2|  KIAA0845 protein [Homo sapiens]
Length = 1034

Score = 322 bits (754), Expect = 3e-87
Identities = 130/188 (69%), Positives = 132/188 (70%), Gaps = 52/188 (27%)

Query: 1 AKSPA EAKSPA EAKSPA K----SPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSPA- 51
AKSPA E KSP +AKSPA K SPA EAKSPEKAKSP AKSPA EAKSPVKEEAKSPA
Sbjct: 580 AKSPA EVKSPEKAKSPA KEEAKSPA EAKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA E 639

Query: 52 -KSPEKAKSPA--EAKSP-----AKSPEKAKSP-----EKAKSP-- 82
KSPEKAKSP EAKSP AKSPEKAKSP EKAKSP
Sbjct: 640 VKSPEKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVK 699

Query: 83 --AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSPA EAKSP-----AKSPVKEEAK 128
AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAK
Sbjct: 700 AEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKTPEKAKSPVKEEAK 759

Query: 129 SPEKAKSP 136
SPEKAKSP
Sbjct: 760 SPEKAKSP 767

Score = 313 bits (732), Expect = 2e-84
Identities = 131/208 (62%), Positives = 132/208 (63%), Gaps = 72/208 (34%)

Query: 1 AKSPA E-----AKSPA EAKSP-----AKSPA E 22
AKSPA E AKSP EAKSP AKSPA E
Sbjct: 546 AKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPA E 605

Query: 23 AKSPEKAKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA--EAKSP--AKSPEK 72
AKSPEKAKSP AKSPA EAKSPVKEEAKSPA KSPEKAKSP EAKSP AKSPEK
Sbjct: 606 AKSPEKAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSPEKAKSPTKEEAKSPEKAKSPEK 665

Query: 73 AKSPEK--AKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP----- 112
AKSPEK AKSP AKSPEKAKSPVK EAKSP AKSPVKEEAKSP
Sbjct: 666 AKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSP 725

Query: 113 --AEAKSP--AKSPVKEEAKSPEKAKSP 136
EAKSP AKSPVKEEAK+PEKAKSP
Sbjct: 726 VKEEAKSPEKAKSPVKEEAKTPEKAKSP 753

Score = 307 bits (717), Expect = 1e-82
Identities = 130/202 (64%), Positives = 130/202 (64%), Gaps = 66/202 (32%)

Query: 1 AKSPA--EAKSPA EAKSP----AKSPA EAKSPEKAKSP----AKSPA EAKSPVKEEAKSP 50
AKSP EAKSPA EAKSP AKSPA E KSPEKAKSP AKSP EAKSP KEEAKSP
Sbjct: 524 AKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSPPEAKSPEKEEAKSP 583

Query: 51 A--KSPEKAKSPA--EAKSP--AKSPEKA-----KSP 76
A KSPEKAKSPA EAKSP AKSPEKA KSP
Sbjct: 584 AEVKSPEKAKSPAKEEAKSPA EAKSPVKEEAKSPA EAKSPVKEEAKSPA EVKSP 643

Query: 77 EAKAKSP-----AKSPEKAKSPVKEEAKSP--AKSPVKEEAKSP-----AEAK 116
EAKAKSP AKSPEKAKSP KEEAKSP AKSPVK EAKSP AEAK
Sbjct: 644 EAKAKSPTKEEAKSPEKAKSPEKAKSPEKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EAK 703

Query: 117 SP--AKSPVKEEAKSPEKAKSP 136
SP AKSPVKEEAKSPEKAKSP
Sbjct: 704 SPEKAKSPVKEEAKSPEKAKSP 725

Score = 280 bits (653), Expect = 2e-74
Identities = 116/159 (72%), Positives = 116/159 (72%), Gaps = 37/159 (23%)

Query: 12 EAKSPA KSPA E--AKSPEK--AKSP----AKSPA EAKSPVKEEAKSPA--KSPEKAKSPA-- 61
E KSP PAE A SPEK AKSP AKSPA EAKSP KEEAKSPA KSPEKAKSPA
Sbjct: 508 ETKSP---PAEEAASPEKEAKSPVKEEAKSPA EAKSPEKEEAKSPA EVKSP EAKSPA KE 564

Query: 62 EAKSP--AKSPEK-----AKSPEKAKSP-----AKSPEKAKSPVKEEAKSP-- 100
EAKSP AKSPEK KSPEKAKSP AKSPEKAKSPVKEEAKSP
Sbjct: 565 EAKSPPEAKSPEKEEAKSPA EVKSP EAKSPA KE EAKSPA EAKSPEKAKSPVKEEAKSPA 624

Query: 101 -AKSPVKEEAKSPA EAKSP--AKSPVKEEAKSPEKAKSP 136
AKSPVKEEAKSPA E KSP AKSP KEEAKSPEKAKSP
Sbjct: 625 EAKSPVKEEAKSPA EVKSP EAKSPA KSP EAKSPEKAKSP 663

Score = 228 bits (531), Expect = 8e-59
Identities = 107/196 (54%), Positives = 116/196 (59%), Gaps = 67/196 (34%)

Query: 1 AKSPA EAKSP--AEAKSP--AKSP--AEAKSPEKAKSP-----AKSPA EAKSPVKEEAKSP 50
AKSP +AKSP AEAKSP AKSP AEAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 674 AKSPEKAKSPVKA EAKSPEKAKSPVKA EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSP 733

Query: 51 -----AKSPEKAKSPA--EAKSP--AKSPEKAKS----- 75
AK+PEKAKSP EAKSP AKSPEKAK+
Sbjct: 734 EKAKSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARS PAD 793

Query: 76 --PEKAKSPAK----SPEKAKSPVKEEAKSP-----AKSPVKEEAKSPA EAKSPA K 120
PEKAKSP K SPEKAKSP+KE+AK+P KSPVKEE K P E K
Sbjct: 794 KFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPVKEEEK-PQEVK---- 848

Query: 121 SPVKEEAKSPEKAKSP 136
VKE K E+ K+P
Sbjct: 849 --VKEPPKAE E E KAP 862

Score = 100 bits (229), Expect = 3e-20
Identities = 89/246 (36%), Positives = 101/246 (41%), Gaps = 122/246 (49%)

Query: 2 KSPA EAKSPA--EAKSPA-----KSPA--EAKSPEKAKSP-----AKSPA-----EA 39
KSP EAK+PA EA+SPA KSP E KSPEKAKSP AK+P E
Sbjct: 776 KSP-EAKTPAKEEARS PADKFPEKAKSPVKEEVKSPEKAKSPLKEDAKAPEKEIPKKEEV 834

Query: 40 KSPVKE-----EAKSPA--KSPEK-----A-----KSP 60
KSPVKE E K+PA K+ EK A K P
Sbjct: 835 KSPVKEEEKPQEVKVKEPPKKAEEEEKAPATPKTEEEKDKSKKEEAPKKEAPKPKVVEEKKEP 894

Query: 61 A-----EAK-----SPAK-----SP-EKA----KSPE--KAKS 81
A EAK +PAK P EK K P+ KAK
Sbjct: 895 AVEKPKESKVEAKKEEAEDKKKVPTPEKEAPAKVEVKEDAKPKEKTEVAKKEPDDAKAKE 954

Query: 82 PAKSPEKAKSPVKEEAKSPAKSPVKEE-AKSPA-E-AKSPAKSPVKEEAKS----P----- 130
P+K EK KE A P K KEE AK P E K+ AK+ KE+ K+ P
Sbjct: 955 PSKPAEK-----KEAA--PEKDDTKEEKAKKPEEKPKTEAKA--KEDDKTLSKEPSKPKA 1005

Query: 131 EKA-KS 135
EKA KS
Sbjct: 1006 EKAES 1011

Score = 97.8 bits (223), Expect = 2e-19
Identities = 41/57 (71%), Positives = 42/57 (73%), Gaps = 9/57 (15%)

Query: 87 EKAKSPVKEEAKSP---AKSPVKEEAKSPA-EAKSP---AKSPVKEEAKSPEKAKSP 136
E+ KSP EEA SP AKSPVKEEAKSPA-EAKSP AKSP E KSPEKAKSP
Sbjct: 507 EETKSPPAEEAASPEKEAKSPVKEEAKSPA-EAKSPEKEEAKSP--AEVKSPEKAKSP 561

☐ >gi|601931|qb|AAA57153.1| neurofilament-H
Length = 511

Score = 317 bits (741), Expect = 1e-85
Identities = 127/172 (73%), Positives = 130/172 (75%), Gaps = 36/172 (20%)

Query: 1 AKSPA--EAKSPA-EAKSPA--KSPA-EAKSPEKAKSP---AKSPA-EAKSPVKEEAKSP-- 50
AKSP EAKSP +AKSP KSPA-EAKSPEKAKSP AKSP +AKSPVKEEAKSP
Sbjct: 194 AKSPEKEEAKSPEKAKSPVEVKSPA-EAKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEK 253

Query: 51 AKSPEKAKSPA--EAKSP-----AKSPEKAKSPEKAKSP---AKSPEKAKSPVK 94
AKSPEKAKSP EAKSP AKSPEKAKSPEKAKSP AKSPEKAKSPVK
Sbjct: 254 AKSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPVK 313

Query: 95 EEAKSP-----AKSPVKEEAKSPA-EAKSP--AKSPVKEEAKSPEKAKSP 136
EEAKSP AKSPVKEEAKSP +AKSP AKSPVKEEAKSPEKAKSP
Sbjct: 314 EEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPEKAKSPVKEEAKSPEKAKSP 365

Score = 312 bits (729), Expect = 4e-84
Identities = 132/219 (60%), Positives = 132/219 (60%), Gaps = 84/219 (38%)

Query: 2 KSPA-EAKSPA-EAKSPA--AKSPA-EAKSPEKAKSPA-----SPA 37
KSPA-EAKSPA-EAKSPA AKSPA-EAKSPEKAKSP K SPA
Sbjct: 93 KSPA-EAKSPA-EAKSPA-EAKSPA-EAKSPEKAKSPEKAKSPVKEEAKSPEKAKSPVEVKSPA 152

Query: 38 EAKSP-----VKEEAKSPA--KSPEKAKSPA--EAKSP-----AKSPEKAKSP- 76
EAKSP VKEEAKSPA KSPEKAKSP EAKSP AKSPEKAKSP
Sbjct: 153 EAKSPEKAKSPVKEEAKSPA-EAKSPEKAKSPEKEEAKSPEKAKSPEKEEAKSPEKAKSPV 212

Query: 77 -----EAKSP---AKSPEKAKSPVKEEAKSP-----AKSPVKEEAKSP- 112
EAKSP AKSPEKAKSPVKEEAKSP AKSPVKEEAKSP